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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/724,797

DATE: 11/14/2001 TIME: 15:08:34

Input Set: A:\2653-40 Sequence Listing.txt
Output Set: N:\CRF3\11142001\I724797.raw

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4 <110> APPLICANT: Jon S. THORSON
 6 <120> TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GENES
        ENCODING FOR BIOSYNTHESIS OF
        CALICHEAMICIN AND SELF-RESISTANCE THERETO
10 <130> FILE REFERENCE: 2653-40
12 <140> CURRENT APPLICATION NUMBER: 09/724,797
                                                       ENTERED
13 <141> CURRENT FILING DATE: 2000-11-28
15 <150> PRIOR APPLICATION NUMBER: 60/111,325
16 <151> PRIOR FILING DATE: 1998-12-07
18 <160> NUMBER OF SEQ ID NOS: 95
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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23 <211> LENGTH: 546
24 <212> TYPE: DNA
25 <213> ORGANISM: Bacteria
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)...(546)
31 <400> SEQUENCE: 1
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36 agc acc gcc gcg aag aag ccg aag ccc ccg aac tac gac ccg ttc gtc
37 Ser Thr Ala Ala Lys Lys Pro Lys Pro Pro Asn Tyr Asp Pro Phe Val
                                   25
               20
                                                                   144
40 cgg cac age gte act gte aag gee gae ege aag ace gee tte aag acg
41 Arg His Ser Val Thr Val Lys Ala Asp Arg Lys Thr Ala Phe Lys Thr
                               40
                                                                   192
44 ttc ctc gaa ggc ttt ccg gag tgg tgg ccg aac aac ttc cgc acc acc
45 Phe Leu Glu Gly Phe Pro Glu Trp Trp Pro Asn Asn Phe Arg Thr Thr
       50
                           55
                                                                   240
48 aaq qtc qqq qcc ccq ctq qqc qtc qac aag aag ggc ggc cgc tgg tac
49 Lys Val Gly Ala Pro Leu Gly Val Asp Lys Lys Gly Gly Arg Trp Tyr
                                           75
52 gag atc gac gag cag ggc gag gag cac acc ttc ggc ctg atc cgg aag
                                                                   288
53 Glu Ile Asp Glu Gln Gly Glu Glu His Thr Phe Gly Leu Ile Arg Lys
                   85
                                       90
                                                                   336
56 qtq qac qaq ccq qac acg ctg gtc atc ggc tgg cgg ctc aac ggc ttc
57 Val Asp Glu Pro Asp Thr Leu Val Ile Gly Trp Arg Leu Asn Gly Phe
60 qqc cqq atc qac ccq qac aac tcg agc gag ttc acc gtg acc ttc gtg
                                                                   384
61 Gly Arg Ile Asp Pro Asp Asn Ser Ser Glu Phe Thr Val Thr Phe Val
                                                 125
62
          115
                              120
64 gcc gac ggc cag aag aac cgg gtg gac gtc gag cac acc cac ttc
                                                                   432
65 Ala Asp Gly Gln Lys Lys Thr Arg Val Asp Val Glu His Thr His Phe
                          135
68 gac cgg atg ggc acc aag cac gcc aag cgg gtc cgc aac ggc atg gac
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Input Set: A:\2653-40 Sequence Listing.txt
Output Set: N:\CRF3\11142001\1724797.raw

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69 Asp Arg Met Gly Thr Lys His Ala Lys Arg Val Arg Asn Gly Met Asp
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72 aag ggc tgg ccg acg atc ctc cag tcg ttc cag gac aag atc gac gag
73 Lys Gly Trp Pro Thr Ile Leu Gln Ser Phe Gln Asp Lys Ile Asp Glu
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74
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76 gaa ggg gcg aag aag tga
77 Glu Gly Ala Lys Lys
78
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82 <211> LENGTH: 181
83 <212> TYPE: PRT
84 <213> ORGANISM: Bacteria
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91 Arg His Ser Val Thr Val Lys Ala Asp Arg Lys Thr Ala Phe Lys Thr
           35
                                40
93 Phe Leu Glu Gly Phe Pro Glu Trp Trp Pro Asn Asn Phe Arg Thr Thr
                           55
95 Lys Val Gly Ala Pro Leu Gly Val Asp Lys Lys Gly Gly Arg Trp Tyr
                       70
97 Glu Ile Asp Glu Gln Gly Glu Glu His Thr Phe Gly Leu Ile Arg Lys
                   85
                                        90
99 Val Asp Glu Pro Asp Thr Leu Val Ile Gly Trp Arg Leu Asn Gly Phe
                100
                                     105
                                                         110
101 Gly Arg Ile Asp Pro Asp Asn Ser Ser Glu Phe Thr Val Thr Phe Val
                                120
            115
                                                     125
103 Ala Asp Gly Gln Lys Lys Thr Arg Val Asp Val Glu His Thr His Phe
                            135
105 Asp Arg Met Gly Thr Lys His Ala Lys Arg Val Arg Asn Gly Met Asp
                        150
                                             155
107 Lys Gly Trp Pro Thr Ile Leu Gln Ser Phe Gln Asp Lys Ile Asp Glu
                                         170
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                    165
109 Glu Gly Ala Lys Lys
110
                180
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114 <211> LENGTH: 1155
115 <212> TYPE: DNA
116 <213> ORGANISM: Bacteria
118 <220> FEATURE:
119 <221> NAME/KEY: CDS
120 <222> LOCATION: (1)...(1155)
122 <400> SEQUENCE: 3
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                                         10
127 atg tet eeg gae gte age ace ege gte tee gee gte etg age agt gge
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Input Set: A:\2653-40 Sequence Listing.txt
Output Set: N:\CRF3\11142001\1724797.raw

128	Met	Ser	${\tt Pro}$	Asp	Val	Ser	Thr	Arg	Val	Ser	Ala	Val	Leu	Ser	Ser	Gly	
129				20					25					30			
131	cgg	ctg	gag	cac	ggg	ccg	acc	gtc	gcc	gag	tac	gag	gcg	gcc	gtg	ggc	144
132	Arg	Leu	Glu	His	Gly	Pro	Thr	Val	Ala	Glu	\mathtt{Tyr}	Glu		Ala	Val	Gly	
133			35					40					45				
135	agt	cgt	atc	ggc	aac	CCC	cgg	gtg	gtc	tcg	gtc	aac	tgc	ggc	acg	gcc	192
136	Ser	Arg	Ile	Gly	Asn	Pro	Arg	Val	Val	Ser	Val	Asn	Cys	Gly	Thr	Ala	
137		50					55					60					
139	ggg	ctc	cac	ctg	gcg	ctg	agc	ctc	gcc	gcg	cgg	ccg	ggg	gcc	ggc	gag	240
140	Gly	Leu	${\tt His}$	Leu	Ala	Leu	Ser	Leu	Ala	Ala	Arg	Pro	Gly	Ala	Gly		
141	65					70					75					80	
143	tcg	gag	cac	gac	ggc	ccg	ggc	gag	gtg	ctc	acc	acg	ccg	ctg	acc	ttc	288
144	Ser	Glu	His	Asp		Pro	Gly	Glu	Val		Thr	Thr	Pro	Leu		Phe	
145					85					90					95		
147	gag	ggc	acg	aac	tgg	ccg	atc	ctc	gcc	aac	ggg	ctg	cgc	atc	cgg	tgg	336
	Glu	Gly	Thr		Trp	Pro	Ile	Leu	Ala	Asn	GTA	Leu	Arg		Arg	Trp	
149				100					105					110			204
									aac								384
	Val	Asp		Asp	Pro	Ala	Thr		Asn	Met	Asp	Leu		Asp	Leu	Ala	
153			115					120					125				420
155	gcg	aag	atc	tcg	CCC	gcc	acc	cgg	gcc	atc	gtg	gtg	gtc	cac	tgg	CTC	432
	Ala			Ser	Pro	Ala		Arg	Ala	тте	val		vaı	HIS	Trp	ren	
157		130					135					140					400
									ctg								480
		Tyr	Pro	Val	Asp		Asn	Arg	Leu	Arg		vaı	vaı	ASP	Arg		
161						150					155	~~~	~~~	+~~	~~~	160	528
163	acg	gcg	gga	tac	gac	cgc	cgc	ccg	ctg	gte	gtg	gag	gac	Crra	geg	Cay	326
	Thr	Ата	GTÀ	туг		Arg	Arg	PIO	Leu		Val	GIU	ASP	Суѕ	175	GIII	
165		.			165	+	~~~	~~~	~~~	170	at a	~~~		a		220	576
16/	gcg	Lgg	ggc	yee	mb~	Lac	Cgg	ggc	gcg Ala	Dro	Tou	99C	mhr	Uic	G1 _v	Agn	370
	Ala	ттр	GIY	180	THE	TYL	ALG	сту	185	PIO	цец	GLY	TIII	190	GIY	ASII	
169	~+ ~	+ ~ ~	~+~		200	200	aaa	aaa	atc	224	ato	cta	2 C C		aac	age	624
172	y LC	Cyc	yuy	Tur	cor	Thr	Glw	λla	Ile	Tive	Tla	Lan	Thr	Thr	Glv	Ser	024
173	Val	Cys	195	тĀт	261	1111	СТУ	200	116	цуз	116	nea	205	1111	OLI	DCI	
	aac	aaa		ata	αtα	cta	CCC		gac	αac	cta	tac		caa	ctc	caa	. 672
									Asp								. 0,2
177	GIY	210	riic	Val	Vul	пси	215	1155	nop.	тор	Lea	220	TIDP		200	9	
	cta		Cac	taa	ctc	aac	_	σασ	cgg	aca	t.ca		caa	atc	acc	aac	720
									Arg								
181		9	5	F		230			5		235		5			240	
		tac	gac	atc	acc		taa	qqc	tac	cqq	ttc	atc	ctc	aac	gag	atc	768
184	Asp	Tyr	Asp	Val	Ala	Glu	Trp	Gly	Tyr	Arg	Phe	Ile	Leu	Asn	Glu	Ile	
185		- 4 -			245		•	-	•	250					255		
	aac	aga	qcq	atc	qqc	ctq	tcc	aac	ctg	gaa	cgc	gtc	gac	gag	ctg	ctg	816
									Leu								
189	-	-		260	-				265		-		-	270			
191	cgc	cgg	cac	cgg	gag	aac	gcc	gcg	ttc	tac	gac	aag	gaa	ctg	gcc	ggc	864
192	Arg	Arg	His	Arg	Glu	Asn	Ala	Ala	Phe	\mathtt{Tyr}	Asp	Lys	Glu	Leu	Ala	Gly	

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Input Set : A:\2653-40 Sequence Listing.txt
Output Set: N:\CRF3\11142001\1724797.raw

193 275 280 285 286 287 286 287 286 287 286 287 286 287 286 287 287 290 291 295 295 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292 292																		
196 fle Asp Gly Val Glu Glu Thr Glu Arg Ala Asp Asp Arg Glu Pro Ala 290 295 300 300 300 199 ttc tgg atg tac ccg ctg aag gtc cgc cgc cgc cgc ctc atg cgc 200 Phe Trp Met Trp Pro Leu Lys Val Arg Asp Arg Pro Ala Phe Met Arg 320 310 310 315 320 320 325 325 325 330 300 325 325 330 300 335 335 325 325 325 330 300 300 335 325 325 330 300 300 335 335 325 325 325 330 300 300 335 335 325 325 325 330 300 300 335 335 325 325 330 300 300 335 335 325 325 330 300 300 335 335 325 325 330 300 300 335 335 325 325 330 300 300 325 335 325 325 330 300 300 325 335 325 325 330 300 300 325 335 325 325 330 300 300 325 335 325 325 330 300 300 325 335 325 325 325 330 300 300 325 335 325 325 330 300 300 325 335 325 325 335 320 300 300 325 335 325 325 325 325 325 325 325 325	193			275					280					285				
197	195	atc	gac	ggc	gtc	gag	cag	acc	gag	cgg	gcc	gac	gac	cgg	gag	CCC	gcg	912
199 ttc tgg atg tac ccg ctg aag gtc cgc gac cgt ccc gcc ttc atg cgc 200 Phe Trp Met Trp Pro Leu Lys Val Arg Asp Arg Pro Ala Phe Met Arg 210 305 310 315 320 320 203 cgg ctg ctc gac gcc ggc atc gcc acc agc gtc gtg tgc gcc cgc aac 204 Arg Leu Leu Asp Ala Gly Ile Ala Thr Ser Val Val Ser Arg Arg Asp 205 325 320 335 335 335 335 335 320 207 gac gcg cac agc tgc gtc gcc gcc gcc acc acc ctc gcc ggc cgc 208 Asp Ala His Ser Cys Val Ala Ser Ala Arg Thr Thr Leu Pro Gly Leu 209 340 345 355 360 365 211 gac cgg gtg gcc gcg acc gcc gtc gtc gcc gcc acc acc ctc gtc gtc gtg tg	196	Ile	Asp	Gly	Val	Glu	Gln	Thr	Glu	Arg	Ala	Asp	Asp	Arg	Glu	Pro	Ala	
200 Phe	197		290					295					300					
200 Phe	199	ttc	taa	atq	tac	ccq	ctq	aaq	gtc	cqc	gac	cgt	ccc	gcc	ttc	atg	cgc	960
201 305																		
203 cgg ctg ctc gac gac gac gac atc gac acc agc gtc gtg tcg cgc egc aac			-					-		-	_							
204 Arg Leu Leu Asp Ala Gly Ile Ala Thr Ser Val Val Ser Arg Arg Arg Ass 325			cta	ctc	gac	qcc	qqc	atc	qcc	acc	agc	qtc	gtg	tcg	cqc	cgc	aac	1008
205	204	Ara	Leu	Leu	Asp	Āla	ĞÎV	Ile	Āla	Thr	Ser	Val	Val	Ser	Arq	Arq	Asn	
207 gac gcg cac age tgc gtc gtc gcg tcg cgc acc acc ctg ccc ggg ctg 208 Asp Ala His Ser Cys Val Ala Ser Ala Arg Thr Thr Leu 750 211 gac cgg gtg gcg gac cgc gtg gtc gac acc atc ccg gtg ggc tgg ttg ccc 212 Asp Arg Val Ala Asp Arg Val Val His Ile Pro Val Gly Trp Trp Leu 350 213 355 215 acc gag gac gac cgc tcc cac gtc gtc gaa acg atc aag tcc ggc tgg 216 Thr Glu Asp Asp Arg Ser His Val Val His Ile Pro Val Gly Trp Trp Leu 370 217 370 375 360 219 tga 220 * 2214 <210> SEQ ID NO: 4 225 <211> LENGTH: 384 226 <212> TYPE: PRT 227 <213> ORGANISM: Bacteria 229 <400> SEQUENCE: 4 230 Met Ala Thr Ser Glu Arg Gly Val Met Ile Pro Leu Ser Lys Val Ala 231 1 5 5 15 246 Arg Ile Gly Asp Pro Arg Val Ala Ala Arg Thr Thr Pro Leu Ser Gly 30 234 Arg Leu Glu His Gly Pro Thr Val Ala Glu Tyr Glu Ala Gly Val Gly 235 35							1				_							
208		gac	aca	cac	адс		atc	aca	t.ca	αcc		acc	acc	cta	ccc	aaa	cta	1056
209																		
211 gac cgg gtg gcg gac cgc gtg gtc cac atc ccg gtg ggc tgg tgg ctc 1104 212 Asp Arg Val Ala Asp Arg Val Val His Ile Pro Val Gly Trp Trp Leu 355 360 365 365 365 365 365 366 365 365 365 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366 366		Mop	21.14	1110			, 42				9					1		
212 ASP Arg Val Ala ASP Arg Val Val His Ile Pro Val Gly Trp Trp Leu 355		a a c	caa	ata			cac	ata	atc		atc	cca	ata	aac		taa	ctc	1104
213																		
215 acc gag gac gac cgc tcc cac gtc gtc gaa acg atc aag tcc ggc tgg 216 Thr Glu Asp Asp Arg Ser His Val Val Glu Thr Ile Lys Ser Gly Trp 217 370 375 380 1155 220 * 224 <210> SEQ ID NO: 4 225 <211> LENGTH: 384 226 <212> TYPE: PRT 227 <213> ORGANISM: Bacteria 229 <400> SEQUENCE: 4 230 Met Ala Thr Ser Glu Arg Gly Val Met Ile Pro Leu Ser Lys Val Ala 231 1 5 5 10 15 232 Met Ser Pro Asp Val Ser Thr Arg Val Ser Ala Val Leu Ser Ser Gly 233 20 5 30 234 Arg Leu Glu His Gly Pro Thr Val Ala Glu Tyr Glu Ala Ala Val Gly 235 35 6 60 236 Ser Arg Ile Gly Asn Pro Arg Val Val Ser Val Asn Cys Gly Thr Ala 237 50 6 60 238 Gly Leu His Leu Ala Leu Ser Leu Ala Ala Arg Pro Gly Ala Gly Glu 239 65 70 70 75 80 240 Ser Glu His Asp Gly Pro Gly Glu Val Leu Thr Thr Pro Leu Thr Phe 241 85 90 95 242 Glu Gly Thr Asn Trp Pro Ile Leu Ala Asn Gly Leu Arg Ile Arg Trp 243 100 100 105 244 Val Asp Val Asp Pro Ala Thr Leu Asn Met Asp Leu Asp Asp Leu Ala 245 115 120 125 246 Ala Lys Ile Ser Pro Ala Thr Arg Ala Ile Val Val Val Asp Arg Ala 247 130 135 165 165 248 Gly Tyr Pro Val Asp Asp Arg Arg Pro Leu Val Val Ola Val Val Val Val Asp Arg Ala 249 145 150 165 250 Thr Ala Gly Tyr Asp Arg Arg Pro Leu Val Val Ola Asp Cys Ala Gln 251 170		ASP	AIG		Ald	изр	лгу	Vai		1113	110	110	V CL			1-5	Dea	
216 Thr Glu Asp Asp Arg Ser His Val Val Glu Thr Ile Lys Ser Gly Trp 217			~~~		~~ ~	000	+ 00	a aa		a+a	~22	200	ato		toc	ααο	taa	1152
217																		1132
219 tga		THE		ASP	ASP	AIG	ser		Vai	vaı	GIU	1111		цуз	SCI	Gry	115	
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230 Met Ala Thr Ser Glu Arg Gly Val Met Ile Pro Leu Ser Lys Val Ala 231 1																		
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233	227 229 230	<213 <400 Met	3> 01 0> 51	RGANI EQUEI	SM: NCE:	4 Glu			Val	Met		Pro	Leu	Ser	Lys		Ala	
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240 Ser Glu His Asp Gly Pro Gly Glu Val Leu Thr Thr Pro Leu Thr Phe 241 85 90 95 242 Glu Gly Thr Asn Trp Pro Ile Leu Ala Asn Gly Leu Arg Ile Arg Trp 243 100 105 110 244 Val Asp Val Asp Pro Ala Thr Leu Asn Met Asp Leu Asp Asp Leu Ala 245 115 120 125 246 Ala Lys Ile Ser Pro Ala Thr Arg Ala Ile Val Val Val His Trp Leu 247 130 135 140 248 Gly Tyr Pro Val Asp Leu Asn Arg Leu Arg Ala Val Val Asp Arg Ala 249 145 150 150 155 160 250 Thr Ala Gly Tyr Asp Arg Arg Pro Leu Val Val Glu Asp Cys Ala Gln 251 165	227 229 230 231 232 233 234 235 236 237	<213 <400 Met 1 Met Arg	3> OH D> SH Ala Ser Leu Arg 50	RGANI Thr Pro Glu 35 Ile	ISM: NCE: Ser Asp 20 His	4 Glu 5 Val Gly Asn	Arg Ser Pro	Gly Thr Thr Arg 55	Arg Val 40 Val	Val 25 Ala Val	10 Ser Glu Ser	Ala Tyr Val	Val Glu Asn 60	Leu Ala 45 Cys	Ser 30 Ala Gly	15 Ser Val Thr	Gly Gly Ala	
241	227 229 230 231 232 233 234 235 236 237	<213 <400 Met 1 Met Arg	3> OH D> SH Ala Ser Leu Arg 50	RGANI Thr Pro Glu 35 Ile	ISM: NCE: Ser Asp 20 His	4 Glu 5 Val Gly Asn	Arg Ser Pro	Gly Thr Thr Arg 55	Arg Val 40 Val	Val 25 Ala Val	10 Ser Glu Ser	Ala Tyr Val	Val Glu Asn 60	Leu Ala 45 Cys	Ser 30 Ala Gly	15 Ser Val Thr	Gly Gly Ala	
242 Glu Gly Thr Asn Trp Pro Ile Leu Ala Asn Gly Leu Arg Ile Arg Trp 243	227 229 230 231 232 233 234 235 236 237 238 239	<213 <400 Met 1 Met Arg Ser Gly 65	3> OH 0> SH Ala Ser Leu Arg 50 Leu	RGANI EQUEN Thr Pro Glu 35 Ile	ISM: NCE: Ser Asp 20 His Gly Leu	4 Glu 5 Val Gly Asn	Arg Ser Pro Pro Leu 70	Gly Thr Thr Arg 55 Ser	Arg Val 40 Val Leu	Val 25 Ala Val Ala	10 Ser Glu Ser	Ala Tyr Val Arg 75	Val Glu Asn 60 Pro	Leu Ala 45 Cys Gly	Ser 30 Ala Gly Ala	15 Ser Val Thr	Gly Gly Ala Glu 80	
243	227 229 230 231 232 233 234 235 236 237 238 239	<213 <400 Met 1 Met Arg Ser Gly 65	3> OH 0> SH Ala Ser Leu Arg 50 Leu	RGANI EQUEN Thr Pro Glu 35 Ile	ISM: NCE: Ser Asp 20 His Gly Leu	4 Glu 5 Val Gly Asn	Arg Ser Pro Pro Leu 70	Gly Thr Thr Arg 55 Ser	Arg Val 40 Val Leu	Val 25 Ala Val Ala	10 Ser Glu Ser	Ala Tyr Val Arg 75	Val Glu Asn 60 Pro	Leu Ala 45 Cys Gly	Ser 30 Ala Gly Ala	15 Ser Val Thr	Gly Gly Ala Glu 80	
244 Val Asp Val Asp Val Asp Pro Ala Thr Leu Asn Met Asp Leu Asp Asp Leu Ala 245 115 246 Ala Lys Ile Ser Pro Ala Thr Arg Ala Ile Val Val Val His Trp Leu 247 130 248 Gly Tyr Pro Val Asp Leu Asn Arg Leu Arg Ala Val Val Asp Arg Ala 249 145 250 Thr Ala Gly Tyr Asp Arg Arg Pro Leu Val Val Glu Asp Cys Ala Gln 251 165	227 229 230 231 232 233 234 235 236 237 238 239 240 241	<213 <400 Met 1 Met Arg Ser Gly 65 Ser	3> OF OS SE Ala Ser Leu Arg 50 Leu Glu	RGANI Thr Pro Glu 35 Ile His	ISM: NCE: Ser Asp 20 His Gly Leu Asp	4 Glu 5 Val Gly Asn Ala Gly 85	Arg Ser Pro Pro Leu 70 Pro	Gly Thr Thr Arg 55 Ser Gly	Arg Val 40 Val Leu Glu	Val 25 Ala Val Ala	10 Ser Glu Ser Ala Leu 90	Ala Tyr Val Arg 75 Thr	Val Glu Asn 60 Pro	Leu Ala 45 Cys Gly Pro	Ser 30 Ala Gly Ala Leu	15 Ser Val Thr Gly Thr 95	Gly Gly Ala Glu 80 Phe	
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246 Ala Lys Ile Ser Pro Ala Thr Arg Ala Ile Val Val Val His Trp Leu 247 130 135 140 248 Gly Tyr Pro Val Asp Leu Asn Arg Leu Arg Ala Val Val Asp Arg Ala 249 Ileu Asp Arg Ala 249 Ileu Asp Arg Arg Pro Leu Val Val Glu Asp Cys Ala Gln 250 Thr Ala Gly Tyr Asp Arg Arg Pro Leu Val Val Glu Asp Cys Ala Gln 175	227 229 230 231 232 233 234 235 236 237 238 239 240 241 242	<213 <400 Met 1 Met Arg Ser Gly 65 Ser	3> OF OS SE Ala Ser Leu Arg 50 Leu Glu	RGANI Thr Pro Glu 35 Ile His	ISM: NCE: Ser Asp 20 His Gly Leu Asp	4 Glu 5 Val Gly Asn Ala Gly 85	Arg Ser Pro Pro Leu 70 Pro	Gly Thr Thr Arg 55 Ser Gly	Arg Val 40 Val Leu Glu	Val 25 Ala Val Ala Val	10 Ser Glu Ser Ala Leu 90	Ala Tyr Val Arg 75 Thr	Val Glu Asn 60 Pro	Leu Ala 45 Cys Gly Pro	Ser 30 Ala Gly Ala Leu	15 Ser Val Thr Gly Thr 95	Gly Gly Ala Glu 80 Phe	
247 130 135 140 248 Gly Tyr Pro Val Asp Leu Asn Arg Leu Arg Ala Val Val Asp Arg Ala 249 145 150 155 160 250 Thr Ala Gly Tyr Asp Arg Arg Pro Leu Val Val Glu Asp Cys Ala Gln 251 165 170 170 175	227 229 230 231 232 233 234 235 236 237 238 240 241 242 243	<213 <400 Met 1 Met Arg Ser Gly 65 Ser Glu	3> OF	RGANI Thr Pro Glu 35 Ile His His	ISM: NCE: Ser Asp 20 His Gly Leu Asp Asn 100	Glu 5 Val Gly Asn Ala Gly 85 Trp	Arg Ser Pro Pro Leu 70 Pro	Gly Thr Thr Arg 55 Ser Gly Ile	Arg Val 40 Val Leu Glu Leu	Val 25 Ala Val Ala Val Ala 105	10 Ser Glu Ser Ala Leu 90 Asn	Ala Tyr Val Arg 75 Thr	Val Glu Asn 60 Pro Thr	Leu Ala 45 Cys Gly Pro Arg	Ser 30 Ala Gly Ala Leu Ile 110	15 Ser Val Thr Gly Thr 95 Arg	Gly Gly Ala Glu 80 Phe	
247 130 135 140 248 Gly Tyr Pro Val Asp Leu Asn Arg Leu Arg Ala Val Val Asp Arg Ala 249 145 150 155 160 250 Thr Ala Gly Tyr Asp Arg Arg Pro Leu Val Val Glu Asp Cys Ala Gln 251 165 170 170 175	227 229 230 231 232 233 234 235 236 237 238 240 241 242 243 244	<213 <400 Met 1 Met Arg Ser Gly 65 Ser Glu	3> OF	RGANI EQUENT Thr Pro Glu 35 Ile His His Thr	ISM: NCE: Ser Asp 20 His Gly Leu Asp Asn 100	Glu 5 Val Gly Asn Ala Gly 85 Trp	Arg Ser Pro Pro Leu 70 Pro	Gly Thr Thr Arg 55 Ser Gly Ile	Arg Val 40 Val Leu Glu Leu Leu	Val 25 Ala Val Ala Val Ala 105	10 Ser Glu Ser Ala Leu 90 Asn	Ala Tyr Val Arg 75 Thr	Val Glu Asn 60 Pro Thr	Leu Ala 45 Cys Gly Pro Arg Asp	Ser 30 Ala Gly Ala Leu Ile 110	15 Ser Val Thr Gly Thr 95 Arg	Gly Gly Ala Glu 80 Phe	
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775 WIG IID GIN WIG III INI WIN GIN WIG EID DEG GIN IIII UIP GIN WEIL	227 229 230 231 232 233 234 235 236 237 238 249 241 242 243 244 245 246 247 248 249 250	<213 <400 Met 1 Met Arg Ser Gly 65 Ser Glu Val Ala Gly 145	3> OI O> SI Ala Ser Leu Arg 50 Leu Glu Gly Asp Lys 130 Tyr	RGANIEQUENT Thr Pro Glu 35 Ile His Thr Val 115 Ile Pro	ISM: NCE: Ser Asp 20 His Gly Leu Asp Asn 100 Asp Ser Val	4 Glu 5 Val Gly Asn Ala Gly 85 Trp Pro Pro Asp Asp	Arg Ser Pro Pro Leu 70 Pro Ala Ala Leu 150	Gly Thr Thr Arg 55 Ser Gly Ile Thr Thr 135 Asn	Arg Val 40 Val Leu Glu Leu 120 Arg	Val 25 Ala Val Ala 105 Asn Ala Leu	10 ser Glu Ser Ala Leu 90 Asn Met Ile Arg Val	Ala Tyr Val Arg 75 Thr Gly Asp Val Ala 155	Val Glu Asn 60 Pro Thr Leu Leu Val 140 Val	Leu Ala 45 Cys Gly Pro Arg Asp 125 Val	Ser 30 Ala Gly Ala Leu Ile 110 Asp His	15 Ser Val Thr Gly Thr 95 Arg Leu Trp Arg	Gly Gly Ala Glu 80 Phe Trp Ala Leu Ala 160	

RAW SEQUENCE LISTINGPATENT APPLICATION: **US/09/724,797**DATE: 11/14/2001
TIME: 15:08:34

Input Set : A:\2653-40 Sequence Listing.txt
Output Set: N:\CRF3\11142001\1724797.raw

185 254 Val Cys Val Tyr Ser Thr Gly Ala Ile Lys Ile Leu Thr Thr Gly Ser 205 195 200 256 Gly Gly Phe Val Val Leu Pro Asp Asp Leu Tyr Asp Arg Leu Arg 210 215 220 258 Leu Arg Arg Trp Leu Gly Ile Glu Arg Ala Ser Asp Arg Ile Thr Gly 230 259 225 235 260 Asp Tyr Asp Val Ala Glu Trp Gly Tyr Arg Phe Ile Leu Asn Glu Ile 250 262 Gly Gly Ala Ile Gly Leu Ser Asn Leu Glu Arg Val Asp Glu Leu Leu 264 Arg Arg His Arg Glu Asn Ala Ala Phe Tyr Asp Lys Glu Leu Ala Gly 275 280 266 Ile Asp Gly Val Glu Gln Thr Glu Arg Ala Asp Asp Arg Glu Pro Ala 290 295 300 268 Phe Trp Met Tyr Pro Leu Lys Val Arg Asp Arg Pro Ala Phe Met Arg 269 305 310 315 270 Arg Leu Leu Asp Ala Gly Ile Ala Thr Ser Val Val Ser Arg Arg Asn 325 330 272 Asp Ala His Ser Cys Val Ala Ser Ala Arg Thr Thr Leu Pro Gly Leu 340 345 274 Asp Arg Val Ala Asp Arg Val Val His Ile Pro Val Gly Trp Trp Leu 355 360 365 276 Thr Glu Asp Asp Arg Ser His Val Val Glu Thr Ile Lys Ser Gly Trp 370 375 380 280 <210> SEQ ID NO: 5 281 <211> LENGTH: 990 282 <212> TYPE: DNA 283 <213> ORGANISM: Bacteria 285 <220> FEATURE: 286 <221> NAME/KEY: CDS 287 <222> LOCATION: (1)...(990) 288 <223> OTHER INFORMATION: biosynthetic gene 290 <400> SEOUENCE: 5 291 gtg ccc aga tcc ctg gtc acc ggc ggc ttc ggc ttc gtc ggc agt cac 48 292 Val Pro Arg Ser Leu Val Thr Gly Gly Phe Gly Phe Val Gly Ser His 295 gtc gtc gaa egg etg gtc ege egg ggt gae gag gtc gtc gtc tac gae 96 296 Val Val Glu Arg Leu Val Arg Arg Gly Asp Glu Val Val Tyr Asp 297 20 25 299 ctc gcc gac ccg ccc gcc ctg gag cac ccg ccg ggc gcg atc cgg 144 300 Leu Ala Asp Pro Pro Pro Asp Leu Glu His Pro Pro Gly Ala Ile Arg 35 301 40 192 303 cac gtc cgc ggc gac gtc cgg gac gcc gac ggg ctg gcg gcc gcc 304 His Val Arg Gly Asp Val Arg Asp Ala Asp Gly Leu Ala Ala Ala Ala 55 307 acc ggc gtg gac gag gtc tac cac ctc gcg gcg gtc gtc ggc gtc gac 240 308 Thr Gly Val Asp Glu Val Tyr His Leu Ala Ala Val Val Gly Val Asp 309 80 65 70

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/724,797

DATE: 11/14/2001 TIME: 15:08:35

Input Set : A:\2653-40 Sequence Listing.txt
Output Set: N:\CRF3\11142001\I724797.raw

L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10